Methods. Premoistened swabs were used to culture sink drains, floor drains, and equipment for CPO. Perirectal swabs were ordered monthly for all patients in non-behavioral health wards. Specimens were plated to CRE- and ESBL-selective media, and colonies identified by MALDI-TOF. The presence of the bla_{KPC} gene was confirmed by PCR. When environmental CPO isolates were detected, EVS procedures and practices were reviewed.

Results. In June 2016, bla_{KPC}+ *Leclercia adecarboxylata* was isolated from an EVS closet floor drain, and in August 2016, from drains in four additional closets. In the previous 10 years, *Leclercia* sp. was isolated just once from a clinical culture. In September 2016, routine surveillance revealed new-onset bla_{KPC}+ *L. adecarboxylata* colonization in a stem cell transplant recipient. Investigation included 33 cultures collected from sink and floor drains, EVS equipment, and other items. EVS equipment, especially mop buckets, were identified as a likely point source due to their use in patient care areas and closets with contaminated floor drains. Among seven mop buckets sampled, one grew bla_{KPC}+ *L. adecarboxylata*. Whole genome sequencing demonstrated genetic relatedness of the *Leclercia* isolates. Floor cleaner was changed to a disinfectant solution. Extensive decontamination of 67 EVS closets and equipment was performed urgently. No further patient or environmental cultures have grown bla_{KPC}+ *L. adecarboxylata*.

Conclusion. The recovery of a highly unusual organism, rarely found in clinical specimens, that was also carrying a bla_{KPC}+ plasmid, allowed us to detect environmental spread of this organism in the hospital. The ability to track this organism using genome sequencing provided strong evidence of the mode of spread, leading to effective remediation. No evidence-based methods exist for remediating drain contamination, which can serve as a potential reservoir for transmission.

Disclosures. **All authors:** No reported disclosures.

996. Bare Below the Elbows: A Randomized Trial to Determine Whether Wearing Short-Sleeved Coats Reduces the Risk for Pathogen Transmission

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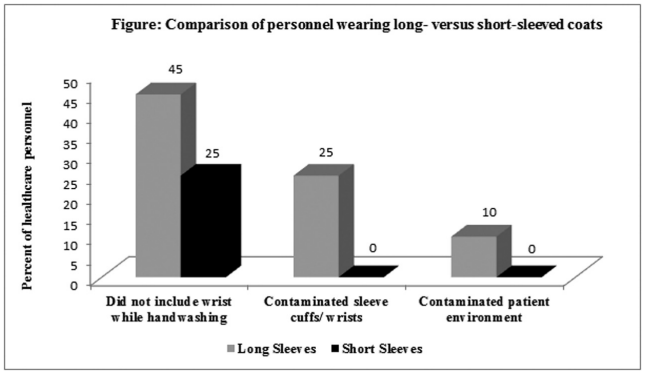
Session: 134. Where Did That Come From? Transmission Risks in Healthcare
Friday, October 6, 2017: 10:30 AM

Background. Physician's white coats are frequently contaminated, but seldom cleaned. Therefore, in the UK, a "bare below the elbows" dress code policy includes a recommendation that personnel wear short sleeves. However, it has not been demonstrated that wearing short sleeves reduces the likelihood of pathogen transmission.

Methods. We conducted a randomized, cross-over trial involving simulated patient care interactions to test the hypothesis that transmission of pathogens occurs less frequently when personnel wear short- vs long-sleeved coats. Healthcare personnel were randomized to wear either long- or short-sleeved white coats while examining a mannequin contaminated with cauliflower mosaic virus DNA followed by examination of an uncontaminated mannequin. We compared the frequency of transfer of the DNA marker with the sleeves and/or wrists and with the uncontaminated mannequin. During work rounds, physicians were observed to determine how often the sleeves of white coats contacted patients or the environment.

Results. During work rounds and simulated examinations, the sleeve cuff of long-sleeved coats frequently contacted the patient/mannequin or environment. Contamination with the DNA marker was detected significantly more often on the sleeves and/or wrists when personnel wore long- vs short-sleeved coats (5 of 20, 25% vs 0 of 20, 0%; P = 0.02). In one of five (20%) instances of sleeve and/or wrist contamination, the DNA marker was transferred to the second mannequin. It was also observed that healthcare personnel were less likely to include their wrist in handwashing between simulations if they were wearing long-sleeved coats.

Conclusion. During simulations of patient care, the sleeve cuff of long-sleeved white coats frequently became contaminated with a viral DNA marker that could be transferred. These results provide support for the recommendation that healthcare personnel wear short sleeves to reduce the risk for pathogen transmission.



Disclosures. **All authors:** No reported disclosures.

997. Defining Aerosol Generating Procedures and Pathogen Transmission Risks in Healthcare Settings

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Session: 134. Where Did That Come From? Transmission Risks in Healthcare
Friday, October 6, 2017: 10:30 AM

Background. Questions remain about the degree to which small particle aerosols are generated during patient care activities and whether such aerosols could transmit viable pathogens to healthcare personnel. This project measured aerosol production during common medical procedures and collected samples for pathogen recovery.

Methods. Six procedures were targeted for aerosol sampling: extubation, bronchoscopy, mechanical ventilation, noninvasive ventilation, suctioning (open or tracheostomy), and nebulized medication administration. Any patient undergoing one of these procedures was eligible for sampling, with a preference for patients with a respiratory viral infection. Baseline samples were collected when possible. Four real-time aerosol characterization instruments were used to detect small particle aerosols generated during procedures. SKC Biosamplers, placed at 3 feet and 6 feet from the patient, were used for pathogen recovery. All samples were subjected to bacterial culture; viral PCR, and viral culture were added depending on the patient's respiratory disease profile.

Results. Samples were collected during extubation ($n = 1$), bronchoscopy ($n = 3$), mechanical ventilation ($n = 13$), noninvasive ventilation ($n = 6$), suctioning ($n = 6$), and nebulized medication administration ($n = 9$). Only nebulized medication administration exhibited differences in particle mass concentration between baseline and procedure aerosol measurements. None of the Biosampler samples were PCR positive for a respiratory virus and none had a positive influenza culture. Five samples had positive bacterial cultures, mainly with common environmental or skin contaminants such as *Micrococcus luteus*, *Staphylococcus pasturei*, and *Bacillus flexus*.

Conclusion. Significant small particle aerosol generation was only seen with nebulized medication administration. No viruses were recovered and minimal viable bacteria were recovered. Additional study is needed to confirm these findings and examine aerosol generation during other procedures commonly considered to be aerosol-generating.

Figure 1: Particle number concentration measurements for baseline and procedure measurements collected for the targeted procedures. Baseline measurements were not collected for continuous procedures (mechanical ventilation and noninvasive ventilation).

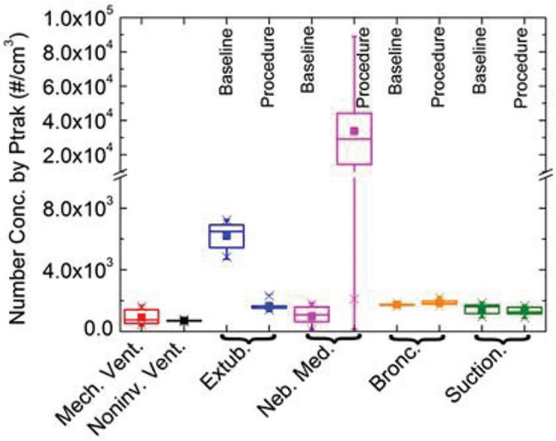
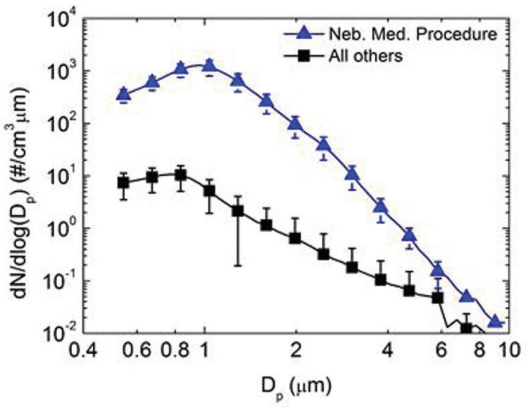


Figure 2: Particle size distribution measurements for nebulized medication samples versus all other procedure samples, combined.



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998. Utility of Routine Genomic Sequencing for Infection Control Surveillance

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Session: 134. Where Did That Come From? Transmission Risks in Healthcare
Friday, October 6, 2017: 10:30 AM

Background. Recent work indicates that comprehensive genomic sequencing can be a highly effective tool in defining the transmission of microbial pathogens. We have studied the utility of the routine use of genomic sequencing for infection control surveillance in an academic medical center.

Methods. The genomes of inpatient and emergency department isolates of *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, and *Enterococcus faecium* were sequenced. Within each species, single-nucleotide polymorphisms (SNP) were identified in the core genome for all isolates using alignment-based methods. The number of SNP differences between isolate pairs was determined and used, in combination with the patient's electronic medical records to identify potential transmission events.

Results. Between September 2016 and March 2017, 388 *S. aureus*, 66 *P. aeruginosa*, 48 *K. pneumoniae*, and 29 *E. faecium* isolates were sequenced from 373 patients. There was variation in the distribution of SNP differences between intrapatient isolates for the four pathogens; with the least variability for *E. faecium* and greatest for *P. aeruginosa*. The majority of the bacterial isolates from separate patients appeared to be genetically unique exhibiting marked SNP differences from other isolates. There were 19 sets of isolates where the SNP variation between interpatient isolates was either comparable to that of intrapatient variation (12) and suggestive of recent transmission events, or with SNP variation somewhat greater than the intrapatient SNP variation (7) suggesting relative relatedness. Only one of the highly related sets had been previously identified by standard infection control surveillance. Likely transmissions appeared to have occurred both in the inpatient and outpatient settings, and the transmission routes were not always apparent.

Conclusion. The routine use of genomic sequencing analysis identified previously unrecognized likely transmission events within the institution's patient population that are of relevance to infection control surveillance. This capacity should significantly enhance our understanding of the epidemiology of hospital acquired infections, and assist in developing and implementing new prevention strategies.

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999. Invasive *Mycobacterium abscessus* Infection after Cardiac Surgery: Epidemiology and Clinical Outcomes

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Session: 134. Where Did That Come From? Transmission Risks in Healthcare
Friday, October 6, 2017: 10:30 AM

Background. We recently mitigated a clonal outbreak of *Mycobacterium abscessus*, including a large cluster of patients who developed invasive infection after exposure to heater-cooler units (HCU) during cardiac surgery. Recent studies have described a small number of *Mycobacterium chimera* infections linked to open-heart surgery; however, little is known about the epidemiology and clinical courses of cardiac surgery patients with invasive infection from rapidly-growing mycobacteria, such as *M. abscessus*.

Methods. We retrospectively collected clinical data from all patients who underwent cardiac surgery at our hospital and had positive cultures for *M. abscessus* from 2013 to 2016. We excluded heart transplant recipients and patients who at time of diagnosis had ventricular assist devices. We analyzed patient characteristics, antibiotic treatment courses, surgical interventions, and clinical outcomes.

Results. Nine cardiac surgery patients who met the case definition developed culture-proven invasive infection from *M. abscessus* (Figure 1). Seven (78%) infections occurred after surgeries that included valve replacement. Median time from suspected inoculation in the operating room to first positive culture was 49 days (interquartile range, 38–115 days). Seven (78%) patients had bloodstream infections, and six (67%) patients had sternal wound infections. Six (67%) patients developed disseminated disease with infection at multiple sites. All patients received combination antimicrobial therapy. The most common majority regimen (n = 6) was imipenem, amikacin, and tigecycline. Four (44%) patients experienced therapy-limiting antibiotic toxicities (Figure 2). Seven (78%) patients were well enough to undergo at least one surgical debridement. Five (56%) patients stopped therapy due to presumed cure, but four (44%) patients had deaths attributable to *M. abscessus* infection.

Conclusion. Invasive *M. abscessus* infection after cardiac surgery was associated with high morbidity and mortality. Most patients underwent surgical debridement and received prolonged three-drug antimicrobial therapy, which was complicated by numerous antibiotic toxicities. Treatment cured five patients, but four patients died from mycobacterial disease.

Figure 1. Clinical courses of 9 patients who developed invasive *Mycobacterium abscessus* infection after cardiac surgery. Incubation period is given from time of suspected innoculation in operating room to time that the first positive culture was obtained.

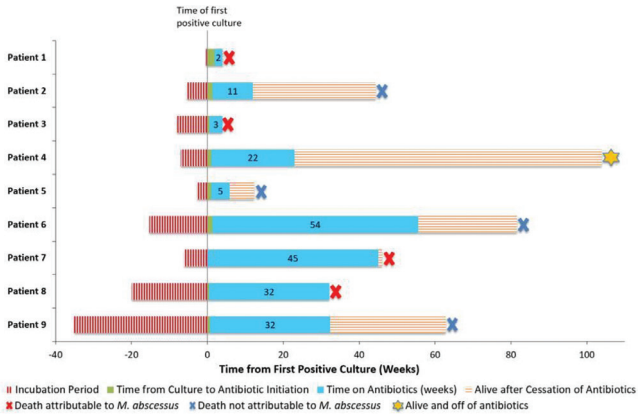
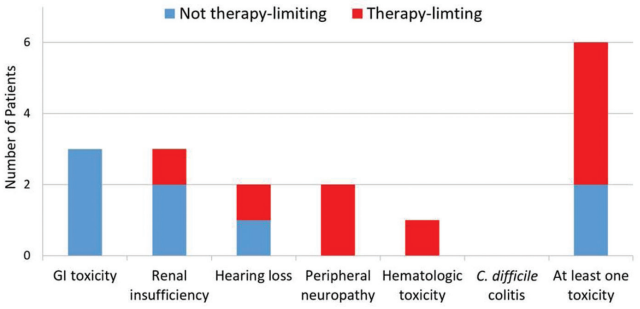


Figure 2. Antibiotic toxicities experienced by 9 cardiac surgery patients treated for invasive *Mycobacterium abscessus* infection. 4 of 6 patients with toxicities required a change in antibiotic regimen.



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1000. Daily Chlorhexidine Bathing in General Hospital Units – Results of the ABATE Infection Trial (Active BAThing to Eliminate Infection)

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Session: 134. Where Did That Come From? Transmission Risks in Healthcare
Friday, October 6, 2017: 10:30 AM

Background. Universal decolonization with daily chlorhexidine (CHG) bathing with and without nasal decolonization has significantly reduced positive MRSA clinical cultures and bloodstream infections in adult ICUs in several clinical trials. We